

Figure 1  
t-PALP  
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1 TTACCAGAACAGCATAACAAGGGCAGGTCTGACTGCAAGCTGGGACTGGGAGGCAGAGCC 60

61 GCCGCCAAGGGGGCCTCGGTAAACACTGGTCGTTCAATCACCTGCAAGACGAAGAGGCA 120

121 AGGATGCTGTTGGCCTGGGTACAAGCATTCTCGTCAGCAACATGCTCCTAGCAGAAGCC 180  
1 M L L A W V Q A F L V S N M L L A E A 19

181 TATGGATCTGGAGGCTGTTTCTGGGACAACGGCCACCTGTACCGGGAGGACCAGACCTCC 240  
20 Y G S G G C F W D N G H L Y R E D Q T S 39

241 CCCGCGCCGGGGCCTCCGCTGCCTCAACTGGCTGGACGCGCAGAGCGGGCTGGCCTCGGCC 300  
40 P A P G L R C L N W L D A Q S G L A S A 59

301 CCCGTGTCGGGGGCGGCAATCACAGTTACTGCCGAAACCCGGACGAGGACCCGCGCGGG 360  
60 P V S G A G N H S Y C R N P D E D P R G 79

361 CCCTGGTGCTACGTCA GTGGCGAGGCCGGCGTCCCTGAGAAACGGCCTTGCGAGGACCTG 420  
80 P W C Y V S G E A G V P E K R P C E D L 99

421 CGCTGTCCAGAGACCACCTCCCAGGCCCTGCCAGCCTTCACGACAGAAATCCAGGAAGCG 480  
100 R C P E T T S Q A L P A F T T E I Q E A 119

481 TCTGAAGGGCCAGGTGCAGATGAGGTGCAGGTGTTTCGCTCCTGCCAACGCCCTGCCCGCT 540  
120 S E G P G A D E V Q V F A P A N A L P A 139

541 CGGAGTGAGGGCGCAGCTGTGCAGCCAGTGATTGGGATCAGCCAGCGGGTGCGGATGAAC 600  
140 R S E A A A V Q P V I G I S Q R V R M N 159

601 TCCAAGGAGAAAAAGGACCTGGGAACCTCTGGGCTACGTGCTGGGCATTACCATGATGGTG 660  
160 S K E K K D L G T L G Y V L G I T M M V 179

661 ATCATCATTGCCATCGGAGCTGGCATCATCTTGGGCTACTCCTACAAGAGGGGAAGGAT 720  
180 I I I A I G A G I I L G Y S Y K R G K D 199

721 TTGAAGAACAGCATGATCAGAAAGTATGTGAGAGGGAGATGCAGCGAATCACTCTGCCC 780  
200 L K E Q H D Q K V C E R E M Q R I T L P 219

781 TTGTCTGCCTTCACCAACCCACCTGTGAGATTGTGGATGAGAAGACTGTCGTGGTCCAC 840  
220 L S A F T N P T C E I V D E K T V V V H 239

841 ACCAGCCAGACTCCAGTTGACCCTCAGGAGGGCAGCACCCCCCTTATGGGCCAGGCCGGG 900  
240 T S Q T P V D P Q E G S T P L M G Q A G 259

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901	ACTCCTGGGGCCTGAGCCCCCAGTGGGCAGGAGCCCATGCAGACACTGGTGCAGGACA	960
260	T P G A *	263
961	CCCCACCCTCCTACAGCTAGGAGGAACTACCACTTTGTGTTCTGGTTAAAACCCTACCAC	1020
1021	TCCCCCGCTTTTGTGGCGAATCCTAGTAAGAGTGACAGAAGCAGGTGGCCCTGTGGGCTG	1080
1081	AGGGTAAGGCTGGGTAGGCTCCTAACAGTGCCTTGTCCATCCCTTGAGACAGATTTTG	1140
1141	TCTGTGGATGGAGACAGTGGCAGCTCCCAQAGTGATGCTGCTGCTAAGGGCTTCCAAACA	1200
1201	TTGCCTGCACCCCTGGAACGAACCAGGGATAGACGGGGAGCTCCCCCAGGCTCCTCTGT	1260
1261	GCTTTACTAAGATGGCTCAGTCTCCACTGTGGGCTTGAGTGGCATACTGTTATTCATG	1320
1321	GTTAAGGTAAAGCAGGTCAAGGGATGGCATTGAAAAAATATATTTAGTTTTTAAATATT	1380
1381	TGGGATGGAACCTCCCTACTGACCTCTGACAACCTGGAACGAGTTTGTACTGAAGTCAGAA	1440
1441	CTTTGGGTGGGAATGAGATCTAGGTTGTGGCTGCTGGTATGCTTCAGCTTGCTGGCAAT	1500
1501	GATGTGCCTTGACAACCGTGGGCCAGGCCTGGGCCAGGGACTCTTCCTGTTTCATAAGG	1560
1561	AAAGGAAGAATTGCACTGAGCATTTCCACTTAGGAAGAGGATAGAGAAGGATCTGCTCCGC	1620
1621	CTTTGGCCACAGGAGCAGAGGCAGACCTGGGATGCCCCAGTTTCTCTTCAGGGATGGATA	1680
1681	GTGACCTGTCTTCATTTTGCACAGGTAAGAGAGTAGTTAGCTAACCTATGGGAATTATAC	1740
1741	TGTGGGGCCTTGTGAGCTGCTTCTAAGAGGCTAACCTGGAACTAAGCTCAGAGGCAAGG	1800
1801	TAATAAAGCACTTCAGGGCTTGCTCCCCAAGTGGGCCTGATTTAGCAGGTGGTCTGCGGG	1860
1861	CGTCCAGGTGAGCACCTTCCTGTAGGGCACTGGGGCTAGGGTCACAGCCCCCTAACTCATA	1920
1921	AAGCAATCAAAGAACCATTAGAAAGGGCTCATTAAGCCTTTTGGACACAGGACCCAGAG	1980
1981	AGGAAAAAGTGACTTGCCCCAAGGTCGTAAGCAAGCTACTGGCATGGCAAGAGCCCAGCTT	2040
2041	CCTGACGGAGCGCAACATTTCTCCACTGCACTGTGCTAGCAGCTCAGCAGGGCCTCTAAC	2100

Figure 1  
t-PALP  
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2101 CTGTGATGTCACACTCAAGAGGCCTTGGCAGCTCCTAGCCATAGAGCTTCCTTTCCAGAA 2160  
2161 CCCTTCCACTGCCCCAATGTGGAGACAGGGGTAGTGGGGCTTTCTATGGAGCCATCTGCT 2220  
2221 TTGGGGACCTAGACCTCAGGTGGTCTCTTGGTGTAGTGATGCTGGAGAAGAGAATATTA 2280  
2281 CTGGTTTCTACTTTTCTATAAAGGCATTTCTCTATAAAAAAAAAAAAAA 2329

20220-16113060

t-PALP  
vs.  
human t-PA

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3 LAWVQAFVLSNMLLAEAY..GSGGCFWDNGHLRYREDQTSAPGLRCLNW. 49
..: :. |:: ..|: |::|::|| |:::.. ..| .|| |
191 YVFKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWN 240
.
50 .....LDAQSGLASAPVSGAGNHSYCRNPDEDPRGPWCYV..... 84
..||. :||. | |. |. |||||::: |||. |
241 SMILIGKVYTAQN..PSAQALGLGKHNYCRNPDGDAK.PWCHVLKNRRLT 287
.
85 SGEAGVPEKRPCEDLRCPETTSQALPAFTTEIQE.....ASEGPGAD 126
.: :||. ..|: :.:. . :. :. |.. |.. :.:
288 WEYCDVPSCSTCGLRQYSQPQFRIKGGFLADIASHPWQAAIFAKHRRSPG 337
.
127 E.....VQVFAPANALPARSEAAAVQPVIGISQVRMNSKEK.. 163
| . :.:|:..: | : :.: | . || ..|.
338 ERFLCGGILISSCWILSAAHCQFERFPPHHLTIVILGRTYRVVPGEEEQKF 387
.
164 .....KDLGTLGYVLGITMMVIIAIG....AGIILGYSYKRGKDL.. 200
|:..: . | :|:..: : : :.: :. :.. ||
388 EVEKYIVHKEFDDDTYDNDIALQLKSDSSRCAQESSVVRTVCLPPADLQ 437
.
201 .....KEQHDQKVCEREMQRITLPLSAFTNPTCEIVDEKTV. 236
|.: :.:. :. :. | : ..|::: :.:|
438 LPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVT 487
.
237 ..VVHTSQTPVDPQEGSTPLMGQAGTPGA 263
.: :.:|. :.:. :. :.:|:
488 DNMLCAGDTRSGGPQANLHDACGDSGGP 516

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# Reference

Figure 3  
t-PALP

